Figure 1

Aligned_sequences:

1: Pcan057

2: Pcan057v1 # Matrix: EDNAFULL # Gap_penalty: 100.0 # Extend_penalty: 0.05 50 1 aaacttcatcaaggtacntaaggttgtaaggttctcggggggtagcggct Pcan057 Pcan057v1 51 tgcacacctcttgaagggcttcarccgggcccctggctccttcaggctgg 100 Pcan057 Pcan057v1 150 101 ctgccttnatccgcttatccaatgattggataacggatgaggggagtctg Pcan057 0 Pcan057v1 200 151 ggtgccaggtgctttgcccgcatggcccatttcagtcacgctgcagtcct Pcan057 0 Pcan057v1 1 250 201 gtcaggaaaaatcagtgttattctcattctacatatgagaaaactgagg Pcan057 0. Pcan057v1 1 300 Pcan057 0 1 Pcan057v1 350 301 agtttcagactccacagtctcttaaccaccaagcagcatgcccagagtag Pcan057 1 Pcan057v1 351 aggtgagaaggaaggagagctgcggtccacatgagcatctggacctag 400 Pcan057 ٥ Pcan057v1 1 450 401 catggacaactcactcctccctggctctcgctttgttcttgttgcgggtg Pcan057 0 1 Pcan057v1 451 tggtggtggtgggactcaaagacggtaaagatagctttctctcccctg 500 Pcan057 Pcan057v1 501 gggaatctgggggttgtttaaaaggcctgctcctcttttagaaggcagga 550 Pcan057 0 Pcan057v1

	o -	
Pcan057	551 gggccccaagggaagcagaaggtgacagaaggggaaagggtcctctgatc	600
Pcan057v1		Ó
Pcan057	601 attgctc	607
Pcan057v1		50
Pcan057	608	607
Pcan057v1	51 agggegegegeeeggeeeceaeceetegeageaeceegegeeeegeee	100
Pcan057	608	607
Pcan057v1	101 teccageegggteeageeggageeatggggeeggageegeagtgageace	150
Pcan057	608	607
Pcan057v1	151 atggagetggeggeettgtgeegetgggggeteeteetegeeetettgee	200
Pcan057	608	607
Pcan057v1	201 ccccggagccgcgagcacccaagtgtgcaccggcacagacatgaagctgc	250
Pcan057	608	607
Pcan057v1	251 ggctccctgccagtcccgagacccacctggacatgctccgccacctctac	300
Pcan057	608	607
Pcan057v1	301 cagggctgccaggtggtgcagggaaacctggaactcacctacct	350
Pcan057	608	607
Pcan057v1	351 caatgccagcctgtccttcctgcaggatatccaggaggtgcagggctacg	400
Pcan057	608	607
Pcan057v1	401 tgctcatcgctcacaaccaagtgaggcaggtcccactgcagaggctgcgg	450
Pcan057	608	607
Pcan057v1	451 attgtgcgaggcacccagctctttgaggacaactatgccctggccgtgct	500
Pcan057	608	607
Pcan057vl	501 agacaatggagacccgctgaacaataccacccctgtcacaggggcctccc	550

Pcan057	608	accccacagagatcttgaaa	627
Pcan057v1	51	caggaggcctgcggagctgcagcttcgaagcctcacagagatcttgaaa	600`
Pcan057	628	ggaggggtcttgatccageggaacccccagetctgctaccaggacacgat	677
Pcan057v1	601	ggaggggtettgatecageggaacececagetetgetaceaggacacgat	650
Pcan057	678	tttgtggaaggacatcttccacaagaacaaccagctggctctcacactga	727
Pcan057v1	651	tttgtggaaggacatcttccacaagaacaaccagctggctctcacactga	700
Pcan057	728	tagacaccaaccgctctcgggcctgccacccctgttctccgatgtgtaag	777
Pcan057v1	701	tagacaccaaccgctctcgggcctgccacccctgttctccgatgtgtaag	750
Pcan057	778	ggctcccgctgctggggagagagttctgaggattgtcagagcctgacgcg	827
Pcan057v1	751	ggctcccgctgctggggagagagttctgaggattgtcagagcctgacgcg	800
Pcan057	828	cactgtctgtgccggtggctgtgcccgctgcaaggggccactgccactg	877
Pcan057v1	801	cactgtctgtgccggtggctgtgcccgctgcaaggggccactgcccactg	850
Pcan057	878	actgctgccatgagcagtgtgctgccggctgcacgggccccaagcactct	927
Pcan057v1	851	actgctgccatgagcagtgtgctgccggctgcacgggccccaagcactct	900
Pcan057	928	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca	977
Pcan057v1	901	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca	950
Pcan057	978	ctgcccagccctggtcacctacaacacagacacgtttgagtccatgccca	1027
Pcan057v1	951	ctgcccagccctggtcacctacaacacagacacgtttgagtccatgccca	1000
Pcan057	102	8 atcccgagggccggtatacattcggcgccagctgtgtgactgcctgtccc	1077
Pcan057v1	100	1 atcccgagggccggtatacattcggcgccagctgtgtgactgcctgtccc	1050
Pcan057	107	8 tacaactacctttctacggacgtgggatcctgcaccctcgtctgccccct	1127
Pcan057v1	105	1 tacaactacctttctacggacgtgggatcctgcaccctcgtctgccccct	1100
Pcan057	112	8 gcacaaccaagaggtgacagcagaggatggaacacagcggtgtgagaagt	1177
Pcan057v1	110	1 gcacaaccaagaggtgacagcagaggatggaacacagcggtgtgagaagt	1150
Pcan057	117	8 gcagcaagccctgtgcccgagtgtgctatggtctgggcatggagcacttg	1227
Pcan057v1	115	1 gcagcaagccctgtgcccgagtgtgctatggtctgggcatggagcacttg	1200

		V	-
Pcan057	1228	cgagaggtgagggcagttaccagtgccaatatccaggagtttgctggctg	1277
Pcan057v1	1201	cgagaggtgagggcagttaccagtgccaatatccaggagtttgctggctg	1250
Pcan057	1278	caagaagatetttgggageettggcatttetgeeggagagetttgatgggg	1327
Pcan057v1	1251	caagaagatetttgggageetggeatttetgeeggagagetttgatgggg	1300
Pcan057	1328	acccagectccaacactgccccgctccagccagagcagctccaagtgttt	1377
Pcan057v1	1301	acccagcctccaacactgccccgctccagccagagcagctccaagtgttt	1350
Pcan057		gagactctggaagagatcacaggttacctatacatctcagcatggccgga	1427
Pcan057v1		gagactctggaagagatcacaggttacctatacatctcagcatggccgga	1400
Pcan057	•	cagcctgcctgacctcagcgtcttccagaacctgcaagtaatccggggac	1477
Pcan057v1		cagectgectgaceteagegtettecagaacetgeaagtaateeggggac	1450
Pcan057		gaattctgcacaatggcgcctactcgctgaccctgcaagggctgggcatc	1527
Pcan057v1		gaattetgeacaatggegeetactegetgaccetgeaagggetgggeate	1500
Pcan057		agetggetgggetgegeteactgagggaactgggeagtggactggeect	1577
Pcan057v1		agetggetgggetgegeteactgagggaactgggcagtggactggccct	1550 1627
Pcan057		catccaccataacacccacctctgcttcgtgcacacggtgccctgggacc	1600
Pcan057v1 Pcan057		agetettteggaaccegcaccaagetetgetecacactgccaaccggcca	1677
Pcan057v1			1650
Pcan057	1678	gaggacgagtgt	1689
Pcan057v1	1651		1700
Pcan057			1689
Pcan057v1	1701	ccagcacacagcagtgcccagggggccctggcagcagcgttcttggactt	1750
Pcan057	1690		1689
Pcan057v1	1751	gtgcagactgcccgtctctgtgcacccttcttgactcagcacagctctgg	1800
Pcan057	1690		1689

Pcan057v1	1801	ctggcttggcctcttggcatggcttctctagctgggtcctacctgccttg	1850
Pcan057	1690	ctggcttggcctcttggcatggcttctctagctgggtcctacctgccttg	1689
Pcan057v1	1851	gratecttecetecetetettetgaaateteagaactetteetete	1900
Pcan057	1690	\$	1689
Pcan057v1		ctacatcggcccacctgtccccaccctccagcccacagccatgcccac	1950
Pcan057	1690		1689
Pcan057v1	1951	agccagttccctggttcacttggacctggggcctcccctaaaagtcccct	2000
Pcan057	1690	gtgggcgagggcctggcctgccaccag	1716
Pcan057v1	2001	geggteeetteeteeteaetgeagtgggegagggeetggeetgeeaecag	2050
Pcan057	1717	ctgtgcgcccgagggcactgctggggtccagggcccaccca	1766
Pcan057v1	2051	ctgtgcgcccgagggcactgctggggtccaggggcccaccca	2100
Pcan057	1767	ctgcagccagttccttcggggccaggagtgcgtggaggaatgccgagtac	1816
Pcan057v1		ctgcagccagttccttcggggccaggagtgcgtggaggaatgccgagtac	2150
Pcan057		tgcaggggctccccagggagtatgtgaatgccaggcactgtttgccgtgc	1866
Pcan057v1	2151	tgcaggggctccccagggagtatgtgaatgccaggcactgtttgccgtgc	2200
Pcan057		caccctgagtgtcagcccagaatggctcagtgacctgttttggaccgga	1916
Pcan057v1		caccetgagtgtcagcccagaatggctcagtgacctgttttggaccgga	2250
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Pcan057v1		tggcccgctgccccagcggtgtgaaacctgacctctcctacatgcccatc	2350
Pcan057		tggaagtttccagatgaggagggcgcatgccagccttgccccatcaactg	2066
Pcan057v1		tggaagtttccagatgaggagggcgcatgccagccttgccccatcaactg	2400
Pcan057		cacccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2116
Pcan057v1	2401	cacccactcctgtgtggacctggatgacaagggctgccccgccgagcaga	2450

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Pcan057	•	gagccagccctctgacgtccatcatctctgcggtggttggcattctgctg	2166
Pcan057v1.		gagccagccctctgacgtccatcatctctgcggtggttggcattctgctg	2500
Pcan057 🐠	2167	gtcgtggtcttgggggtggtctttgggatcctcatcaagcgacggcagca	2216
Pcan057v1	2501	gtcgtggtcttggggtctttgggatcctcatcaagcgacggcagca	2550
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Pcan057v1		gaagatccggaagtacacgatgcggagactgctgcaggaaacggagctgg	2600
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Pcan057	2317	atcctgaaagagacggagctgaggaaggtgaaggtgcttggatctggcgc	2366
Pcan057v1	2651	atcctgaaagagacggagctgaggaaggtgaaggtgcttggatctggcgc	2700
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Pcan057	2517	atatgtctcccgccttctgggcatctgcctgacatccacggtgcagctgg	2566
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Pcan057v1	2901	tgacacagcttatgccctatggctgcctcttagaccatgtccgggaaaac	2950
Pcan057	2617	cgcggacgcctgggctcccaggacctgctgaactggtgtatgcagattgc	2666
Pcan057v	2951	cgcggacgcctgggctcccaggacctgctgaactggtgtatgcagattgc	3000
Pcan057	2667	caaggggatgagctacctggaggatgtgcggctcgtacacagggacttgg	2716
Pcan057v1	3001	caaqqqqatqaqctacctqqaqqatqtqcqqctcqtacacaqqqacttqq	3050

Pcan057	2717	ccgctcggaacgtgctggtcaagagtcccaaccatgtcaaaattacagac	2766
Pcan057v1	3051	ccgctcggaacgtgctggtcaagagtcccaaccatgtcaaaattacagac	3100
Pcan057	2767	ttcgggctggctcggctgctggacattgacgagacagagtaccatgcaga	2816
Pcan057v1	3101	ttcgggctggctggctgctggacattgacgagacagagtaccatgcaga	3150
Pcan057	2817	tgggggcaaggtgcccatcaagtggatggcgctggagtccattctccgcc	2866
Pcan057v1	3151	tgggggcaaggtgcccatcaagtggatggcgctggagtccattctccgcc	3200
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Pcan057v1	3301	gatccctgacctgctggaaaagggggagcggctgccccagcccccatct	3350
Pcan057	3017	gcaccattgatgtctacatgatcatggtcaaatgttggatgattgactct	3066
Pcan057v1	3351	gcaccattgatgtctacatgatcatggtcaaatgttggatgattgactct	3400
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Pcan057v1	3401	gaatgteggeeaagatteegggagttggtgtetgaatteteeegeatgge	3450
Pcan057	3117	cagggacccccagcgctttgtggtcatccagaatgaggacttgggcccag	3166
Pcan057v1	3451	cagggacccccagcgctttgtggtcatccagaatgaggacttgggcccag	3500
Pcan057	3167	ccagtcccttggacagcaccttctaccgctcactgctggaggacgatgac	3216
Pcan057v1	3501	ccagtcccttggacagcaccttctaccgctcactgctggaggacgatgac	3550
Pcan057	3217	atgggggacctggtggatgctgaggagtatctggtaccccagcagggctt	3266
Pcan057v1		atgggggacctggtggatgctgaggagtatctggtaccccagcagggctt	3600
Pcan057		cttctgtccagaccctgccccgggcgctggggcatggtccaccacaggc	3316
Pcan057v1		cttctgtccagaccctgccccgggcgctggggcatggtccaccacaggc	3650
Pcan057		accgcagctcatctaccaggagtggcggtggggacctgacactagggctg	3366
Pcan057v1	3651	accgcagctcatctaccaggagtggcggtggggacctgacactagggctg	3700

Pcan057	3367	gagecetetgaagaggaggeeeceaggteteeactggeaceeteegaagg	3416
Pcan057v1	3701	gagecetetgaagaggececeaggteteeaetggeaceeteegaagg	3750
Pcan057	3417	gg@ggctccgatgtatttgatggtgacctgggaatgggggcagccaagg	3466
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Pcan057v1	3851	gaggaccccacagtacccctgccctctgagactgatggctacgttgccc	3900
Pcan057	3567	cctgacctgcagccccagcctgaatatgtgaaccagccag	3616
Pcan057v1	3901	cctgacctgcagccccagcctgaatatgtgaaccagccag	3950
Pcan057	3617	cccagccccttcgcccgagagggccctctgcctgctgcccgacctgct	3666
Pcan057v1	3951	cccagccccttcgcccgagagggccctctgcctgctgcccgacctgct	4000
Pcan057	3667	ggtgccactctggaaagggccaagactctctccccagggaagaatggggt	3716
Pcan057v1	4001	ggtgccactctggaaagggccaagactctctccccagggaagaatggggt	4050
Pcan057	3717	cgtcaaagacgtttttgcctttgggggtgccgtggagaaccccgagtact	3766
Pcan057v1	4051	cgtcaaagacgtttttgcctttgggggtgccgtggagaaccccgagtact	4100
Pcan057	3767	tgacaccccagggaggagctgcccctcagccccaccctcctcctgccttc	3816
Pcan057v1	4101	tgacaccccagggaggagctgcccctcagccccaccctcctcctgccttc	4150
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Pcan057vl	4151	agcccagccttcgacaacctctattactgggaccaggacccaccagagcg	4200
Pcan057	3867	gggggctccacccagcaccttcaaagggacacctacggcagagaacccag	3916
Pcan057v1	4201	gggggctccacccagcaccttcaaagggacacctacggcagagaacccag	4250
Pcan057	3917	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	3966
Pcan057v1	4251	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	4300
Pcan057	3967	aagccctgatgtgtcctcagggagcagggaaggcctgacttctgctggca	4016
Pcan057v1	4301	aagccctgatgtgtcctcagggagcagggaaggcctgacttctgctggca	4350

Pcan057	4017	tcaagaggtgggaġggccctccgaccacttccaggggaacctgccatgcc	4066
Pcan057vl	4351	tcaagaggtgggagggccctccgaccacttccaggggaacctgccatgcc	4400
Pcan057	4067	aggaacctgtcctaaggaaccttccttcctgcttgagttcccagatggct	4116
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Pcan057vl	4451	ggaaggggtccagcctcgttggaagaggaacagcactggggagtctttgt	4500
Pcan057	4167	ggattctgaggccctgcccaatgagactctagggtccagtggatgccaca	4216
Pcan057v1	4501	ggattctgaggccctgcccaatgagactctagggtccagtggatgccaca	4550
Pcan057	4217	gcccagcttggccctttccttccagatcctgggtactgaaagccttaggg	4266
Pcan057v1	4551	gcccagcttggccctttccttccagatcctgggtactgaaagccttaggg	4600
Pcan057	4267		4316
Pcan057v1		aagctggcctgagagggaagcggccctaagggagtgtctaagaacaaaa	4650
Pcan057		gcgacccattcagagactgtccctgaaacctagtactgcccccatgagg	4366
Pcan057v1	4651	gcgacccattcagagactgtccctgaaacctagtactgccccccatgagg	4700
Pcan057	4367		4416
Pcan057v1		aaggaacagcaatggtgtcagtatccaggctttgtacagagtgcttttct	4750
Pcan057		gtttagtttttacttttttgttttgttttttaaagatgaaataaagac	4466
Pcan057v1		gtttagtttttacttttttgttttgtttttttaaagatgaaataaagac	4800
Pcan057		ccagggggagaatgggtgttgtatggggaggcaagtgtggggggtccttc 	4516
Pcan057v1		ccagggggagaatgggtgttgtatggggaggcaagtgtggggggtccttc	4850
Pcan057		tccacacccactttgtccatttgcaaatatattttggaaaaca 4559	
Pcan057v1	4851	tccacacccactttgtccatttgcaaatatattttggaaaaca 4893	

Figure 2

# Aligned_sequ	ienc	es: 2	•
# 1: Pcan057.			2.00
# 2: Pcan057v	l.aa		
# Matrix: EBLO	MUSC		
# Gap penalty:	: 10	0.0	
# Extend pena:			
		=======================================	
	•		·
Pcan057.aa	1		0
Pcan057v1.aa	. 1	MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLY	50
Pcan057.aa	1		0
Pcan057v1.aa	51	QGCQVVQGNLELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLR	100
Pcan057.aa	1	MGLSFRLHSLLTTKQ: .	15
Pcan057v1.aa	101	IVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL	145
Pcan057.aa	16	HAQSRGEKEGESCGPHEHLDLAWTTHSSLALALFLLRVWWWWDSKTVKIA	65
Pcan057v1.aa	146		14,5
Pcan057.aa		FSPPWGIWGLFKRPAPLLEGRRAPREAEGDRRGKGPLIIAHPTEILKGGV	115
Pcan057v1.aa	146		153
Pcan057.aa	116	LIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR	165
Pcan057v1.aa	154	LIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSPMCKGSR	203
Pcan057.aa	166	CWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL	215
Pcan057v1.aa	204	CWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL	253
		ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY	269
Pcan057v1.aa	254	ACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY	30:
Pcan057.aa	266	LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREV	31!
Pcan057v1.aa	304	LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREV	35
Pcan057.aa	316	RAVTSANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL	36
Pcan057v1.aa	354	RAVISANIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL	40

Pcan057.aa	366	EEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWL	415
Pcan057v1.aa	404	EEITGYLYISAWPDSLPDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWL	453
Pcan057.aa	416	GERSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE	465
Pcan057v1.aa	454	GLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE	503
Pcan057.aa	466	CVGEGLACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPRE	515
Pcan057v1.aa	504	CGKTGSPVCALPICQHTAVPRGPWQQRSWTCADCPSLCTLLDSAQLWLAW	553
Pcan057.aa	516	YVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG	565
Pcan057v1.aa	554	PLGMASLAGSYLPWHPSLPLCF	575
Pcan057.aa	566	VKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS	615
Pcan057v1.aa	576		575
Pcan057.aa	616	IISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPS	665
Pcan057v1.aa	576		575
Pcan057.aa	666	GAMPNQAQMRILKETELRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIK	715
Pcan057v1.aa	576		575
Pcan057.aa	716	VLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPY	765
Pcan057v1.aa	576		575
Pcan057.aa	766	GCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLV	815
Pcan057v1.aa	576		575
Pcan057.aa	816	KSPNHVKITDFGLARLLDIDETEYHADGGKVPIKWMALESILRRRFTHQS	865
Pcan057v1.aa	576		575
Pcan057.aa	866	DVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYM	915
Pcan057v1.aa	576		575
Pcan057.aa	916	IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDST	965
Pcan057v1.aa	576		575
Pcan057.aa	966	FYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHRHRSSSTR	1015

Pcan057v1.a	a 576		57.5
Pcan057.aa	1016	SGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLGMGAAKGLQSLPT	1065
Pcan057v1.a	a 576		575
Pcan057.aa	1066	HDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR	1115
Pcan057v1.a	a 576		575
Pcan057.aa	1116	EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGA	1165
Pcan057v1.a	a 576		575
Pcan057.aa	1166	APQPHPPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV	1215
Pcan057v1.a	a 576		575
Pcan057.aa	1216	PV 1217	
Pcan057v1.a	a 576	575 ·	

356

400

406

450

456

500

506

Figure 3

Pro108

Prol77

Pro108

Pro177

Pro108

Pro177

Pro108

Aligned sequences: 1: Pro108 · 2: Pro177 Matrix: EDNAFULL Gap_penalty: 100.0 Extend_penalty: 0.01 gcacga 6 1 Pro108 1 gggagggataggacggggagacaaagaaaggggtgcggcagcactgccag 50 Pro177 56 7 gggaagaggtgatccgacccggggaaggtcgctgggcagggcgagttgg Pro108 100 51 gggaagagggtgatccgacccggggaaggtcgctgggcagggcgagttgg Pro177 57 gaaageggeageeeeggeeeeegeageeeetteteeteetteteee 106 Pro108 101 gaaagcggcagccccgccgccccgcagccccttctcctcctttctccc 150 Pro177 156 107 acgtcctatctgcctctcgctggaggccaggccgtgcagcatcgaagaca Pro108 151 acgtcctatctgcctctcgctggaggccaggccgtgcagcatcgaagaca 200 Pro177 157 ggaggaactggagcctcattggccggcccgggggggcgccggcctcgggctta 206 Pro108 201 ggaggaactggagcctcattggccggcccgggcgccggcctcgggctta 250 Pro177 207 aataggageteegggetetggetgggaceegacegetgeeggeegete 256 Pro108 300 Pro177 306 257 ccgctgctcctgccgggtgatggaaaaccccagcccggccgccgccctgg Pro108 350 301 ccgctgctcctgccgggtgatggaaaaccccagcccggccgccgccctgg Pro177

357 cctcttgggggagagtccatctgttccgccagagccccggccaaatacag

401 cctcttgggggagagtccatctgttccgccagagccccggccaaatacag

407 catcaccttcacgggcaagtggagccagacggccttccccaagcagtacc

451 catcacetteacgggcaagtggagccagacggcettececaagcagtace

457 ccctgttccgccccctgcgcagtggtcttcgctgctgggggccgcgcat

Pro177	501	ccctgttccgccccctgcgcagtggtcttcgctgctgggggccgcgcat	550
Pro108		ageteegaetacageatgtggaggaagaaccagtacgtcagtaacggget	556
Pro177	,551	ageteegaetacageatgtggaggaagaaccagtaegteagtaaeggget	600
`Pro108	557	gcgcgactttgcggagcgcggcgaggcctgggcgctgatgaaggagatcg	606
Pro177	601	gcgcgactttgcggagcgcggcgaggcctgggcgctgatgaaggagatcg	650
Pro108	·	aggcggcggggggggcgctgcagagcgtgcacgcggtgttttcggcgccc	656
Pro177	651	aggeggeggggggggegetgeagagegtgeaegaggtgtttteggegeee	700
Pro108		gccgtccccagcggcaccgggcagacgtcggcggagctggaggtgcagcg	706
Pro177	701	gccgtccccagcggcaccgggcagacgtcggagctggaggtgcagcg	750
Pro108	707	caggcactcgctggtctcgtttgtggtgcgcatcgtgcccagccccgact	756
Pro177	751	caggcactcgctggtctcgtttgtggtgcgcatcgtgcccagccccgact	800
Pro108	757	ggttcgtgggcgtggacagcctggacctgtgcgacggggaccgttggcgg	806
Pro177	801		850
Pro108	807	gaacaggeggcgctggacctgtacccctacgacgccgggacggacagcgg	856
Pro177	851		900
Pro108	857	cttcaccttctcctccccaacttcgccaccatcccgcaggacacggtga	906
Pro177	901		950
Pro108	907	ccgagataacgtcctctctcccagccacccggccaactccttctactac	956
Pro177	951		1000
Prol08	957	ccgcggctgaaggccctgcctcccatcgccagggtgacactggtgcggct	1006
Pro177	1001	ccgcggctgaaggccctgcctcccatcgccagggtgacactgctgcggct	1050
Pro108	1007	gcgacagagccccagggccttcatccctcccgccccagtcctgcccagca	1056
Pro177	1051	gcgacagagccccagggccttcatccctcccgccccagtcctgcccagca	1100
Pro108	1057	gggacaatgagattgtagacagcgcct	1083
Pro177	1101	gggacaatgagattgtagacagcgcctcaggtaacggacatacaggtcac	1150

Pro108	1084	1083
Pro177	1151 atgggacacacagcagccccgaaccctgccacagggcgaccaccaaaccc	1200
Pro108	1084	1083
Pro177	1201 gaacctaaggctctgagaaattccaagtagggattcgtagtgcgtactgc	1250
Pro108	1084	1083
Pro177	1251 aagatggtgcctagaagatttaggattctgttgattcacacactgaagat	1300
Pro108	1084	1083
Pro177	1301 gtgactcttgcacattatttgcagttgaaagcatcttacagggccacagc	1350
Pro108	1084	1083
Pro177	1351 ccagaggaaagaatgaaaggaggctccagacagtacctgagagactctgt	1400
Pro108	1084	1083
Pro177	1401 cctgtcagacacgcacccacaggtgacctgtgtgtcacagctgacaagga	1450
Pro108	1084	1083
Pro177	1451 agcttgctaggatggccctgtgtggccaccgggtgacagctatgctgcag	1500
Pro108	1084	1083
Pro177	1501 ggcacetgtgggggtetegggacecagecacacacageteggggetetg	1550
Pro108	1084	1083
Pro177	1551 ctcacaggcgccttggcctggggcggggcaggtgctgatgagcattctcc	1600
Pro108	1084	1083
Pro177	1601 tagetettecaggeacetgetggacagggcaggetgggaacgetggggce	1650
Pro108	1084	1083
Pro177	1651 gagtggcagttccctccctactcagctgggtggcagccactggcctcacg	1700
Pro108	1084	1083
Pro177	1701 gagcgcctgtggtctggagcgcattgctgggtcgtgggtcagggcctgtt	1750
Pro108	1084	1083

Pro177	1751 ggetetgggtetetgggteteacetgatatgggtgtgggacagteagtgt	1800
Pro108	1084	1083
Pro177	1801 aggccccagacaacagcggacttcagactttcccgaggaggaactggagc	1850
Pro108	1084	1083
Pro177	1851 ccaccaacctggccatgggccccgtcgtcctccaccctccatgttgctgg	1900
Pro108	1084	1083
Pro177	1901 ctggagttgaggcaggtacggggccgcccacacctgcccccaagccat	1950
Pro108	1084	1083
Pro177	1951 gtggtagggacagatgtcgtcttgaggagcagcagtaattacaagcttac	2000
Pro108	1084	1083
Pro177	2001 tgtcagccgtccctggaagcaagggccaggtcaggtcag	2050
Pro108	1084	1083
Pro177	2051 cctggctggcgggaaccactccccagacagagactgtgcccagtcctggg	2100
Pro108	1084	1083
Pro177	2101 tecetecteatttgggatgaactgggeeteeetgtgeeageeteggtget	2150
Pro108	1084	1083
Pro177	2151 gcccctgcccagtgcaggcttgggctcctcactcatttgtccacgcggat	2200
Pro108	1084	1083
Pro177	2201 gccccattccaagcagatgtccccgagccacttacccaacaggcagacgt	2250
Pro108	1084	1083
Pro177	2251 gccagcactgttcgtggtgtgcaactggtctggcgggaagagcccctcgt	2300
Pro108	1084	1083
Pro177	2301 gggcagagggtccagagggtgcggtttgccccacatttgggggcactgg	2350
Pro108	1084	1083
Pro177	2351 gccacagtgggcaggggagcacgtggccagtgccctgggtctgccacgat	2400

•		•	
Pro108	1084		1083
Pro177		grgggagtreeaceaceacagggaerrgageggeagereeggererraeg	2450
Pro108	1084		1083
Pro177	2451	tagaaacgcgcaactccagtccctaggttgtgtccgaggttgctatggtg	2500
Pro108	1084		1083
Pro177	2501	ccatcccatcttgccgctcactctgcgactgtgcggagaaacgcaagtgc	2550
Pro108	1084		1083
Pro177		ccccgaagggtgggcgtggcctctgatgaatgcacacgttggtgggaggt	2600
Pro108	1084		1083
Prol77	2601	ggcttccgtttgtacgaagcgcctcttcacgcgagcgttcacctcggtct	2650
Pro108	1084	cagttccagaaacgccgctggactgcgaggtctcc	1118
Pro177	2651	ccctttgcttggtccagttccagaaacgccgctggactgcgaggtctcc	2700
Pro108	1119	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	1168
Pro177	2701	ctgtggtcgtcctggggactgtgcggaggccactgtgggaggctcgggac	2750
Pro108	1169	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	1218
Pro177	2751	caagagcaggactcgctacgtccgggtccagcccgccaacaacgggagcc	2800
Pro108	1219	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	1268
Pro177	2801	cctgccccgagctcgaagaagaggctgagtgcgtccctgataactgcgtc	2850
Pro108	1269	taagaccagagccccgcagcccctgggg-cccccggagccatggggtgtc	1317
Pro177	2851	taagaccagagccccgcagcccctggggccccccggagccatggggtgtc	2900
Pro108	1318	gggggctcctgtgcaggctcatgctgcaggcggccga-ggcacagggggt	1366
Pro177	2901	gggggctcctgtgcaggctcatgctgcaggcggccgagggcacagggggt	2950
Pro108	1367	ttcgcgctgctcctgaccgcggtgaggccgcgccgaccatctctgcactg	1416
Pro177	2951	ttcgcgctgctcctgaccgcggtgaggccgccgaccatctctgcactg	3000

Pro108	1417	aagggccctctggtggccggcacgggcattgggaaacagcctcctctt	2466
Pro177	3001	aagggccctctggtggccggcacgggcattgggaaacagcctcctcttt	3050
Pro108	1467	cccaaccttgcttcttaggggccccgtgtcccgtctgctctcagcctcc	1516
Pro177	3051	cccaaccttgcttcttaggggccccgtgtcccgtctgctctcagcctcc	3100
Pro108	1517	tcctcctgcaggataaagtcatccccaaggctccagctactctaaattat	1566
Pro177	3101	tcctcctgcaggataaagtcatccccaaggctccagctactctaaattat	3150
Pro108	1567	ggtctccttataagttattgctgctccaggagattgtccttcatcgtcca	1616
Pro177	3151	-gtctccttataagttattgctgctccaggagattgtccttcatcgtcca	3199
Pro108	1617	ggggcctggctcccacgtggttgcagatacctcagacctggtgctctagg	1666
Pro177	3200	ggggcctggctcccacgtggttgcagatacctcagacctggtgctctagg	3249
Pro108	1667	ctgtgctgagcccactctcccgagggcgcatccaagcgggggccacttga	1716
Pro177	3250	ctgtgctgagcccactctcccgagggcgcatccaagcgggggccacttga	3299
Pro108	1717	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	1766
Pro177	3300	gaagtgaataaatggggcggtttcggaagcgtcagtgtttccatgttatg	3349
Pro108	1767	gatctctctgcgtttgaataaagactatctctgttgctcac 180	7
Pro177	3350	gatetetetgegtttgaataaagaetatetetgttgeteaaaaa 339	3

Figure 4

# 1: PRO108 # 2: PRO177 # Matrix: I # Gap_penal # Extend_pe	3.aa 7.aa EBLOS Ity: enalt	100.0						•		•
PRO108.aa		MENPSPAAALG	11111		111111			111111	11	50
PRO177.aa	1	MENPSPAAAL	KALCA	LLLATI	GAAGQP	LGGESI	CSARAPA	KYSITFT	'GK	50
PRO108.aa	51	WSQTAFPKQYI	LFRPP	AQWSSL	LGAAHS	SDYSMWI	RKNQYVS	NGLRDFA	ER 	100
PRO177.aa	51	WSQTAFPKQYI	LFRPP	AQWSSI	LGAAHS	SDYSMWI	KNOYVS	NGLRDFA	ER	100
PRO108.aa		GEAWALMKEII	11111	!!!!.		11111	111111	11111	11	150
PRO177.aa	101	GEAWALMKEI	EAAGEA	LOSVHE	EVFSAPA	VPSGTG	OTSAELE	VQRRHSI	.VS	150
PRO108.aa		FVVRIVPSPD		111111					.	200
PRO177.aa	151	FVVRIVPSPD	VFVGVD	SLDLCI	GDRWRE	ÖŸYTDT.	YPYDAGI	DSGFTFS	SSP	200
PRO108.aa		NFATIPQDTV				111111	111111	:		250
PRO177.aa	201	NFATIPODTV	reitss	SPSHP	NSFYYP	RLKALP	PIARVTI	LLRLRQSI	PRA	250
PRO108.aa	251	FIPPAPVLPS	RDNEIV	DSASVI	PETPLDO	EVSLWS	SWGLCGG	HCGRLG	rks	300
PRO177.aa	251	FIPPAPVLPS	RDNEIV	DSASGI	NGHTGHM	GHTAAP	NPATGRI	PPNPNLRI	Ĺ	298
PRO108.aa	301	RTRYVRVQPA	NNGSPC	PELEE	EAECVPI	NCV	331			
PRO177.aa	299						298			•

Figure 5

# Aligned_sequences: 2	
# 1: PRO108.aa	
# [©] 2: PRO177.orf	
# Matrix: EBLOSUM62	
# Gap_penalty: 100.0	
# Extend_penalty: 0.01	
#======================================	
PRO108.aa 1	0
PRO177.orf 1 RCDSCTLFAVESILQGHSPEERMKGGSRQYLRDSVLSDTHPQVTCVSQLT	50
PRO108.aa 1	0
PRO177.orf 51 RKLARMALCGHRVTAMLQGTCGGLGTQPPHSSGLCSQAPWPGAGQVLMSI	100
PRO108.aa 1	0
PRO177.orf 101 LLALPGTCWTGQAGNAGAEWQFPPYSAGWQPLASRSACGLERIAGSWVRA	150
PRO108.aa 1	0
PRO177.orf 151 CWLWVSGSHLIWVWDSQCRPQTTADFRLSRGGTGAHQPGHGPRRPPPSML	200
PRO108.aa 1	0
PRO177.orf 201 LAGVEAGTGPPHTCPPSHVVGTDVVLRSSSNYKLTVSRPWKQGPGQVRQE	250
PRO108.aa 1	0
PRO177.orf 251 AAWLAGTTPQTETVPSPGSLLIWDELGLPVPASVLPLPSAGLGSSLICPR	300
PRO108.aa 1	0
PRO177.orf 301 GCPIPSRCPRATYPTGRRASTVRGVQLVWREEPLVGRGSREVRFAPHLGA	350
PRO108.aa 1	0
PRO177.orf 351 LGHSGQGSTWPVPWVCHDVGVPPPQGLERQLRLLRRNAQLQSLGCVRGCY	400
PRO108.aa 1 MEN:	3
PRO177.orf 401 GAIPSCRSLCDCAEKRKCPRRVGVASDECTRWWEVASVCTKRLFTRAFTS	450
PRO108.aa 4 PSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQ .	53
PRO177.orf 451 VSPLL	455
PRO108.aa 54 TAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA	103

		TAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA	103
PRO177.orf	456		455
PRO108.aa	104	WALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSFVV	153
PRO177.orf	456		455
PRO108.aa	154	RIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFA	203
PRO177.orf	456		455
PRO108.aa	204	TIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPRAFIP	253
PRO177.orf	456		455
PRO108.aa	254	PAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTR	303
PRO177.orf	456		490
PRO108.aa	304	YVRVQPANNGSPCPELEEEAECVPDNCV 331	
PRO177.orf	491	YVRVQPANNGSPCPELEEEAECVPDNCV 518	